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DATE: Tuesday, February 15, 2005

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	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND		
☐	L1	clostrid$.clm. and perfring$.clm.	168
☐	L2	L1 and promoter.clm.	9
☐	L3	L1 and promoter.clm.	9
☐	L4	clostrid$ near6 perfring$	2854
☐	L5	L4 near50 promoter	4
☐	L6	L5 not l3	3

END OF SEARCH HISTORY

☐ 1. 20040029201. 11 Jul 03. 12 Feb 04. Identification of targets of antimicrobial compounds. Fan, Frank, et al. 435/7.23; G01N033/574.

☐ 2. 20040029129. 25 Oct 02. 12 Feb 04. Identification of essential genes in microorganisms. Wang, Liangsu, et al. 435/6; 435/183 435/252.33 435/254.2 435/320.1 435/325 435/419 435/69.1 530/350 536/23.2 C12Q001/68 C07H021/04 C12N001/20 C12N009/00 C12P021/02 C12N001/21 C07K014/47 C12N005/04 C12N001/18.

☐ 3. 20030186281. 20 Dec 02. 02 Oct 03. Modified tetracycline repressor protein compositions and methods of use. Hillen, Wolfgang. 435/6; 435/191 435/252.3 435/252.31 435/320.1 435/69.1 435/7.32 536/23.2 C12Q001/68 G01N033/554 G01N033/569 C07H021/04 C12N009/06 C12N001/21 C12P021/02 C12N015/74.

☐ 4. 20030124507. 13 Mar 02. 03 Jul 03. Method of generating conditionally expressed mutant cells using expressible antisense sequences. Marra, Andrea, et al. 435/4; 435/252.3 435/471 435/6 C12Q001/00 C12Q001/68 C12N015/74 C12N001/21.

☐ 5. 20030027286. 21 Dec 01. 06 Feb 03. Bacterial promoters and methods of use. Haselbeck, Robert, et al. 435/69.6; 435/219 435/252.3 435/320.1 435/6 536/23.2 C07H021/04 C12P021/04 C12N009/50 C12Q001/68 C12N001/21 C12N015/74.

☐ 6. 20020086310. 30 Aug 01. 04 Jul 02. Identification of targets of antimicrobial compounds. Fan, Frank, et al. 435/6; 435/32 C12Q001/68 C12Q001/18.

☐ 7. 6780447. 19 Feb 02; 24 Aug 04. Bacteriocin-containing sorbic acid product as addition to feedstuffs in agricultural livestock rearing. Raczek; Nico N.. 426/61;. A23K001/18.

☐ 8. 5955368. 06 Apr 98; 21 Sep 99. Expression system for clostridium species. Johnson; Eric A., et al. 435/488; 435/252.3 435/320.1 435/476 536/23.1 536/24.1. C12N001/21 C12N015/70 C12N015/74 C12N015/64.

☐ 9. 5004692. 15 Dec 87; 02 Apr 91. Cloning and expression of phosopholipase C genes. Tso; J. Yun, et al. 435/183; 435/195 435/252.3 435/252.33 435/320.1 435/358 435/365 435/367 536/23.2 536/23.7. C12N009/00 C12N009/14.

☐ 1. 20040029201. 11 Jul 03. 12 Feb 04. Identification of targets of antimicrobial compounds. Fan, Frank, et al. 435/7.23; G01N033/574.

☐ 2. 20040029129. 25 Oct 02. 12 Feb 04. Identification of essential genes in microorganisms. Wang, Liangsu, et al. 435/6; 435/183 435/252.33 435/254.2 435/320.1 435/325 435/419 435/69.1 530/350 536/23.2 C12Q001/68 C07H021/04 C12N001/20 C12N009/00 C12P021/02 C12N001/21 C07K014/47 C12N005/04 C12N001/18.

☐ 3. 20030186281. 20 Dec 02. 02 Oct 03. Modified tetracycline repressor protein compositions and methods of use. Hillen, Wolfgang. 435/6; 435/191 435/252.3 435/252.31 435/320.1 435/69.1 435/7.32 536/23.2 C12Q001/68 G01N033/554 G01N033/569 C07H021/04 C12N009/06 C12N001/21 C12P021/02 C12N015/74.

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☐ 5. 20030027286. 21 Dec 01. 06 Feb 03. Bacterial promoters and methods of use. Haselbeck, Robert, et al. 435/69.6; 435/219 435/252.3 435/320.1 435/6 536/23.2 C07H021/04 C12P021/04 C12N009/50 C12Q001/68 C12N001/21 C12N015/74.

☐ 6. 20020086310. 30 Aug 01. 04 Jul 02. Identification of targets of antimicrobial compounds. Fan, Frank, et al. 435/6; 435/32 C12Q001/68 C12Q001/18.

☐ 7. 6780447. 19 Feb 02; 24 Aug 04. Bacteriocin-containing sorbic acid product as addition to feedstuffs in agricultural livestock rearing. Raczek; Nico N.. 426/61;. A23K001/18.

☐ 8. 5955368. 06 Apr 98; 21 Sep 99. Expression system for clostridium species. Johnson; Eric A., et al. 435/488; 435/252.3 435/320.1 435/476 536/23.1 536/24.1. C12N001/21 C12N015/70 C12N015/74 C12N015/64.

☐ 9. 5004692. 15 Dec 87; 02 Apr 91. Cloning and expression of phosopholipase C genes. Tso; J. Yun, et al. 435/183; 435/195 435/252.3 435/252.33 435/320.1 435/358 435/365 435/367 536/23.2 536/23.7. C12N009/00 C12N009/14.

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L6: Entry 3 of 3 File: DWPI Mar 6, 2003

DERWENT-ACC-NO: 1999-217498
DERWENT-WEEK: 200433

TITLE: Clostridium beta2 toxin gene promoter and signal sequence - useful against toxins from Clostridium perfringens

Basic Abstract Text (1):
The nucleic acid of the Clostridium perfringens beta 2 toxin gene promoter comprising at least part of sequence (I) (given in the specification), is new.
ATTTGGGATA TCTTAAATTT AGCACAGAAG AATGTTTAAA TGAAATAAAG ATAATAAAAA GATATATTAA
TTATATAGCT GAAAATTTAT AATTATATGA TAAGTATAGT TAATAAATAA AAAGTGTTCT CGGGGGACAC
TTTTTTGTTT TAAAAAGGAA AATATAAATA AAATTTAGAT AAAAGTGTAA AATAATTATT TTTATTTTAA
ATTTGTTAAA AATTTGATAT AATTGAATTG TAAAAAAAAT TTCAGGGGGG AATATAAATG AAAATTATTA
TTTCAAAGTT TACTGTAATT TTTATGTTTT CATGTTTTCT TATTGTT (I). NOTE: The last 60 bases of (I) encode the first 20 amino acids of the signal peptide (II).

Previous Doc Next Doc Go to Doc#

File 53:FOODLINE(R): Science Sight 1972-2005/Feb 14
(c) 2005 LFRA
*File 53: Price change effective Jan 1, 2005. Enter HELP RATES 53 for details.
File 149:TGG Health&Wellness DB(SM) 1976-2005/Feb W1
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(c) 2005 EPO

Set	Items	Description

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Set	Items	Description
S1	203	(CLOSTRID? OR PERFRINGEN?)/TI AND PROMOTER?/TI
S2	75	RD (unique items)

?t s2/9/6 12 13 14 15 16 17 23 66 67 68

2/9/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

13159543 PMID: 8828224
An upstream activating sequence containing curved DNA involved in activation of the Clostridium perfringens **plc** promoter .
Matsushita C; Matsushita O; Katayama S; Minami J; Takai K; Okabe A
Department of Microbiology, Kagawa Medical School, Japan.
Microbiology (Reading, England) (ENGLAND) Sep 1996, 142 (Pt 9) p2561-6, ISSN 1350-0872 Journal Code: 9430468
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The plc gene, which encodes phospholipase C (alpha-toxin) of Clostridium perfringens, possesses three poly(A) tracts forming an intrinsically curved DNA region immediately upstream of the promoter. The in vivo transcriptional activity of the plasmid-borne plc gene was stimulated by this curved-DNA-containing sequence, depending on its proper linear and rotational orientation. The in vitro transcriptional activity of the plc gene was also stimulated by the upstream sequence. In addition, the stimulatory effect of the sequence and the degree of DNA bending were greater at lower temperature, as was demonstrated by both in vitro and in vivo transcription assays, and a gel-mobility assay, respectively. A similar temperature effect was also observed with the chromosomal plc gene. These observations suggest that the upstream DNA curvature per se stimulates the initiation of transcription of the plc gene, possibly through direct contact with RNA polymerase.
Tags: Support, Non-U.S. Gov't
Descriptors: *Clostridium perfringens--genetics--GE; *Phospholipase C --genetics--GE; Base Sequence; Chromosome Mapping; Chromosomes--genetics --GE; Chromosomes--physiology--PH; DNA--physiology--PH; Gene Expression Regulation, Bacterial; Molecular Sequence Data; Mutagenesis, Insertional; Mutagenesis, Site-Directed; Nucleic Acid Conformation; Plasmids--genetics --GE; Plasmids--physiology--PH; Promoter Regions (Genetics); Sequence Deletion; Temperature; Transcription, Genetic
CAS Registry No.: 0 (Plasmids); 9007-49-2 (DNA)
Enzyme No.: EC 3.1.4.3 (Phospholipase C)

Record Date Created: 19970113
Record Date Completed: 19970113

2/9/12 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10260070 PMID: 7960138
Expression from the Clostridium perfringens **cpe** promoter **in C.** perfringens **and Bacillus subtilis.**
Melville S B; Labbe R; Sonenshein A L
Department of Molecular Biology and Microbiology, Tufts University School of Medicine, Boston, Massachusetts 02111.
Infection and immunity (UNITED STATES) Dec 1994, 62 (12) p5550-8, ISSN 0019-9567 Journal Code: 0246127
Contract/Grant No.: GM42219; GM; NIGMS; P30 DK34928; DK; NIDDK
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Clostridium perfringens is a source of food poisoning in humans and animals because of production of a potent enterotoxin (CPE). To study the regulation of the cpe gene in C. perfringens, we cloned and sequenced the cpe promoter regions and N-terminal domains from three strains. The cpe promoter region from one strain contained a 45-bp insertion compared with previously published sequences. This insertion was also found in two (of five) other Cpe+ strains. cpe gene expression in C. perfringens was measured by using translational fusions of each promoter type to the Escherichia coli gusA gene, which codes for beta-glucuronidase. For either promoter type, cpe-gusA expression was undetectable throughout exponential growth but increased dramatically at the beginning of the stationary phase. To measure cpe expression in Bacillus subtilis, cpe-gusA fusions were integrated into the B. subtilis chromosome. Both types of promoter exhibited moderate expression during exponential growth; cpe expression increased threefold at the beginning of the stationary phase. Transcriptional start sites were determined by primer extension and in vitro transcription assays. For C. perfringens, both types of promoter gave the same 5' end, 197 bp upstream of the translation start (50 bp downstream of the 45-bp insertion). In B. subtilis, however, the 5' end was internal to the 45-bp insertion, suggesting the use of a different promoter than that utilized by C. perfringens.
Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Descriptors: *Clostridium perfringens--genetics--GE; *Enterotoxins --genetics--GE; *Gene Expression Regulation, Bacterial; *Promoter Regions (Genetics)--genetics--GE; Bacillus subtilis--genetics--GE; Base Sequence; Cell-Free System; Cloning, Molecular; Clostridium perfringens--growth and development--GD; DNA, Recombinant; Electroporation; Enterotoxins --biosynthesis--BI; Glucuronidase--biosynthesis--BI; Glucuronidase --genetics--GE; Molecular Sequence Data; Polymerase Chain Reaction; RNA, Messenger--genetics--GE; Raffinose--pharmacology--PD; Recombinant Fusion Proteins--biosynthesis--BI; Sequence Analysis, DNA; Spores, Bacterial--drug effects--DE; Spores, Bacterial--growth and development--GD; Starch --pharmacology--PD; Transcription, Genetic; Translation, Genetic
Molecular Sequence Databank No.: GENBANK/U11257; GENBANK/U11259; GENBANK/U11294
CAS Registry No.: 0 (DNA, Recombinant); 0 (Enterotoxins); 0 (RNA, Messenger); 0 (Recombinant Fusion Proteins); 0 (enterotoxin, Clostridium); 512-69-6 (Raffinose); 9005-25-8 (Starch)
Enzyme No.: EC 3.2.1.31 (Glucuronidase)
Gene Symbol: cpe
Record Date Created: 19941229
Record Date Completed: 19941229

2/9/13 (Item 13 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

10170067 PMID: 8058826
A Clostridium perfringens **vector for the selection of** promoters .
Matsushita C; Matsushita O; Koyama M; Okabe A
Department of Microbiology, Kagawa Medical School, Japan.
Plasmid (UNITED STATES) May 1994, 31 (3) p317-9, ISSN 0147-619X Journal Code: 7802221
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

A promoter selection vector for Clostridium perfringens genes was constructed from a C. perfringens-Escherichia coli shuttle vector, pJIR418. The plasmid carries a promoterless chloramphenicol acetyltransferase gene (catP), derived from pIP401, downstream of the multiple cloning sites of pUC18. When a promoter region of the phospholipase C gene was inserted into one of the cloning sites, derivatives of C. perfringens strain 13 carrying the resultant plasmid acquired resistance to chloramphenicol. This plasmid should be useful reporter system for C. perfringens genes.

Tags: Support, Non-U.S. Gov't
Descriptors: *Clostridium perfringens--genetics--GE; *Genetic Vectors; *Plasmids; *Promoter Regions (Genetics); Base Sequence; Blotting, Northern; Chloramphenicol O-Acetyltransferase--biosynthesis--BI; Chloramphenicol O-Acetyltransferase--genetics--GE; Chloramphenicol O-Acetyltransferase --metabolism--ME; Cloning, Molecular--methods--MT; DNA Primers; Escherichia coli; Genes, Bacterial; Molecular Sequence Data; RNA, Messenger--analysis --AN; RNA, Messenger--biosynthesis--BI; Restriction Mapping
CAS Registry No.: 0 (DNA Primers); 0 (Genetic Vectors); 0 (Plasmids) ; 0 (RNA, Messenger)
Enzyme No.: EC 2.3.1.28 (Chloramphenicol O-Acetyltransferase)
Gene Symbol: catP
Record Date Created: 19940914
Record Date Completed: 19940914

2/9/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08801833 PMID: 1981087
Studies on Clostridium **acetobutylicum glnA** promoters **and antisense RNA.**
Janssen P J; Jones D T; Woods D R
Department of Microbiology, University of Cape Town, Rondebosch, South Africa.
Molecular microbiology (ENGLAND) Sep 1990, 4 (9) p1575-83, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The Clostridium acetobutylicum glnA gene has two transcript start sites under the control of promoters p1 and p2. Initiation of transcription was regulated by nitrogen and a downstream region was implicated in the regulation of transcript initiation by nitrogen in Escherichia coli. Putative antisense RNA was produced from a single downstream transcript start site under the control of p3. An up-promoter mutation in p3 resulted in lower levels of glutamine synthetase (GS) activity. Putative antisense RNA had a role in down-regulating GS expression but was not involved in regulation by nitrogen. Deletion of downstream inverted repeat sequences resulted in very low levels of GS activity.

Descriptors: *Clostridium--genetics--GE; *Gene Expression Regulation, Bacterial; *Glutamate-Ammonia Ligase--genetics--GE; *Promoter Regions

(Genetics); *RNA, Antisense--genetics--GE; Base Sequence; Clostridium --enzymology--EN; Escherichia coli--genetics--GE; Genes, Bacterial; Glutamate-Ammonia Ligase--metabolism--ME; Molecular Sequence Data; Mutation ; Nitrogen--pharmacology--PD; RNA, Antisense--metabolism--ME; Repetitive Sequences, Nucleic Acid; Transcription, Genetic
CAS Registry No.: 0 (RNA, Antisense); 7727-37-9 (Nitrogen)
Enzyme No.: EC 6.3.1.2 (Glutamate-Ammonia Ligase)
Gene Symbol: glnA
Record Date Created: 19910325
Record Date Completed: 19910325

2/9/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07999446 PMID: 2463955
Identification and characterization of Clostridium **difficile** promoter **element that is functional in Escherichia coli.**
Dailey D C; Schloemer R H
Department of Microbiology and Immunology, Indiana University School of Medicine, Indianapolis 46223.
Gene (NETHERLANDS) Oct 30 1988, 70 (2) p343-50, ISSN 0378-1119 Journal Code: 7706761
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The promoter element involved in the expression of a previously characterized cloned clostridial antigen was isolated and characterized. A restriction fragment containing the promoter element of the Clostridium difficile insert was cloned using the promoter probe vector, pGA46. Subclones of the clostridial DNA insert in pGA46 were then analyzed by nucleotide sequencing and by S1 nuclease experiments. The clostridial promoter element exhibits a high degree of homology with typical Escherichia coli promoter elements. This sequence probably represents a unique class of clostridial promoter elements which, given their ability to function in E. coli and C. difficile, can be used in the construction of a shuttle vector capable of gene expression in E. coli and C. difficile.
Descriptors: *Clostridium--genetics--GE; *Escherichia coli--genetics--GE; *Promoter Regions (Genetics); *Transformation, Genetic; Aspergillus Nuclease S1; Base Sequence; Blotting, Southern; Cloning, Molecular; Electrophoresis, Agar Gel; Endonucleases--diagnostic use--DU; Gene Expression Regulation; Genetic Vectors; Plasmids; RNA, Bacterial--isolation and purification--IP; Restriction Mapping; Tetracycline Resistance --genetics--GE
Molecular Sequence Databank No.: GENBANK/M22864
CAS Registry No.: 0 (Genetic Vectors); 0 (Plasmids); 0 (RNA, Bacterial)
Enzyme No.: EC 3.1.- (Endonucleases); EC 3.1.30.1 (Aspergillus Nuclease S1)
Record Date Created: 19890302
Record Date Completed: 19890302

2/9/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07931034 PMID: 2460717
Studies of UV-inducible promoters **from** Clostridium perfringens **in vivo and in vitro.**
Garnier T; Cole S T
Biochimie des Regulations Cellulaires, Institut Pasteur, Paris, France.
Molecular microbiology (ENGLAND) Sep 1988, 2 (5) p607-14, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Expression of a 4 kb segment of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens is inducible by UV-irradiation. DNA sequence analysis revealed that this region contains three genes: uviA, uviB and bcn encoding the bacteriocin BCN5. Biochemical studies with mRNAs showed that expression was controlled at the transcriptional level and that the genes were organized in two independent transcriptional units, uviAB and bcn, both directed by tandem promoters inducible by UV light. The bcn gene is transcribed from three promoters (P1, P2, P3) while transcription of uviAB is directed by two promoters (P4, P5). With the exception of P4, which bears some resemblance to the consensus eubacterial promoter sequence, none of these promoters was recognized in vitro by the major forms of RNA polymerase from C. perfringens, Bacillus subtilis or Escherichia coli. Promoters P1, P3 and P5, which show striking homology with each other, contain unusual sequences in the '-35' and '-10' regions known to be recognized by RNA polymerase and this might indicate positive control.

Tags: Support, Non-U.S. Gov't

Descriptors: *Clostridium perfringens--genetics--GE; *Gene Expression Regulation; *Promoter Regions (Genetics); Amino Acid Sequence; Base Sequence; Clostridium perfringens--enzymology--EN; DNA-Directed RNA Polymerases--biosynthesis--BI; DNA-Directed RNA Polymerases--isolation and purification--IP; Molecular Sequence Data; Plasmids; RNA, Bacterial --biosynthesis--BI; RNA, Messenger--biosynthesis--BI; Restriction Mapping; Ultraviolet Rays

Molecular Sequence Databank No.: GENBANK/J03309; GENBANK/J03310

CAS Registry No.: 0 (Plasmids); 0 (RNA, Bacterial); 0 (RNA, Messenger)

Enzyme No.: EC 2.7.7.6 (DNA-Directed RNA Polymerases)

Record Date Created: 19881220

Record Date Completed: 19881220

2/9/17 (Item 17 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07187369 PMID: 3733758

In vivo and in vitro transcription of the Clostridium **pasteurianum ferredoxin gene. Evidence for "extended"** promoter **elements in gram-positive organisms.**

Graves M C; Rabinowitz J C

Journal of biological chemistry (UNITED STATES) Aug 25 1986, 261 (24) p11409-15, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: AI6712; AI; NIAID; AM2109-28; AM; NIADDK

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Analysis of Clostridium pasteurianum genomic DNA indicates that the ferredoxin (Fd) gene is present in a single copy. The cloned Fd gene previously described (Graves, M.C., Mullenbach, G. T., and Rabinowitz, J. C. (1985) Proc. Natl. Acad. Sci. U. S. A. 82, 1653-1657) was used to map in vivo and in vitro synthesized Fd transcripts. The in vivo mRNA was sized in two ways: by Northern hybridization analysis, and more directly from the known DNA sequence after the 5'- and 3'-termini were identified. The 5'-end was determined by primer extension-dideoxy sequencing and the 3'-end by S1 nuclease mapping. The monocistronic Fd mRNA contains about 255 nucleotides and, thus, is one of the shortest bacterial mRNAs yet described. We also examined the Fd transcripts produced by Escherichia coli transformed with the plasmid containing the Fd gene. E. coli RNA polymerase most likely recognizes the same promoter (P1) as the clostridial polymerase, and furthermore, efficiently uses an additional promoter (P2) that is poorly

recognized by the normal host enzyme. For comparison, in vitro transcripts were generated by E. coli and Bacillus subtilis RNA polymerases. In vitro, only promoter P1 is used by either E. coli or B. subtilis RNA polymerase. The 3'-end of each of the four types of transcripts occurs essentially at the same location and maps to within a large dyad symmetry element. Comparison of the Fd promoter with other Gram-positive promoters reveals that some sequences outside of the traditional Pribnow and -35 regions are conserved. This analysis indicates that an "extended" promoter recognition site may be required in these organisms.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Clostridium--genetics--GE; *Ferredoxins--genetics--GE; *Promoter Regions (Genetics); *Transcription, Genetic; Base Sequence; Electrophoresis, Polyacrylamide Gel; Nucleic Acid Conformation; Nucleic Acid Hybridization; RNA, Messenger--metabolism--ME

Molecular Sequence Databank No.: GENBANK/M11214; GENBANK/M13633; GENBANK/M13682

CAS Registry No.: 0 (Ferredoxins); 0 (RNA, Messenger)

Record Date Created: 19860919

Record Date Completed: 19860919

2/9/23 (Item 6 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

0010820891 BIOSIS NO.: 199799454951

The level of expression of alpha-toxin by different strains of Clostridium perfringens **is dependent on differences in** promoter **structure and genetic background**

AUTHOR: Bullifent Helen L; Moir Anne; Awad Milna M; Scott Paul T; Rood Julian I; Titball Richard W

AUTHOR ADDRESS: Defence Evaluation and Res. Agency, CBD Porton Down, Salisbury, Wiltshire SP4 0JQ, UK**UK

JOURNAL: Anaerobe 2 (6): p365-371 1996 1996

ISSN: 1075-9964

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The control of expression of the alpha-toxin gene (cpa or plc) of Clostridium perfringens has been studied in three strains shown to have high (NCTC8237), intermediate (strain 13) and low (NCTC8533) phospholipase C activity in the culture supernatant. The phospholipase C activity was shown to be related to cpa mRNA levels. Primer extension studies were performed to locate the cpa promoter regions in strains NCTC8237 and 13. Differences in promoter sequences could account for the differences in alpha-toxin production between strains 13 and NCTC8237. In contrast, the differences in alpha-toxin production between strains NCTC8237 and NCTC8533 were unlikely to be due to promoter differences because the upstream promoter-containing sequences were identical in these strains. The recombinant plasmid carrying the NCTC8237 cpa gene was introduced into strains 13 and NCTC8533. The level of production of the alpha-toxin was 16-fold higher in strain 13, indicating the presence of strain-dependant regulatory systems.

REGISTRY NUMBERS: 9001-86-9Q: PHOSPHOLIPASE C; 63551-76-8Q: PHOSPHOLIPASE C

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Enzymology--Biochemistry and Molecular Biophysics; Genetics; Molecular Genetics--Biochemistry and Molecular Biophysics; Physiology; Toxicology

BIOSYSTEMATIC NAMES: Endospore-forming Gram-Positives--Eubacteria, Bacteria, Microorganisms

ORGANISMS: endospore-forming gram-positive rods and cocci (Endospore-forming Gram-Positives); Clostridium perfringens (Endospore-forming Gram-Positives)

COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms

CHEMICALS & BIOCHEMICALS: PHOSPHOLIPASE C
MISCELLANEOUS TERMS: ALPHA-TOXIN; GENE EXPRESSION; MOLECULAR GENETICS; PHOSPHOLIPASE C; PROMOTER MAPPING; STRAIN-NCTC8237; STRAIN-NCTC8533; STRAIN-13; TOXICOLOGY
CONCEPT CODES:
10064 Biochemistry studies - Proteins, peptides and amino acids
10300 Replication, transcription, translation
10808 Enzymes - Physiological studies
22501 Toxicology - General and methods
31000 Physiology and biochemistry of bacteria
31500 Genetics of bacteria and viruses
BIOSYSTEMATIC CODES:
07810 Endospore-forming Gram-Positives

2/9/66 (Item 8 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0080240 DBR Accession No.: 88-11089
Isolation of promoter **from 2 anaerobic bacteria - cloning** Clostridium **absonum and Bacteroides thetaiotaomicron DNA in Escherichia coli; DNA sequence**
AUTHOR: Roberts I; Hylemon P B; Holmes W M
CORPORATE SOURCE: Department of Microbiology, Medical College of Virginia, Virginia Commonwealth University, Richmond, Virginia 23298-0678, USA.
JOURNAL: Microbios (54, 219, 87-99) 1988
CODEN: MCBIA7
LANGUAGE: English
ABSTRACT: DNA fragments were cloned from 2 anaerobes, Clostridium absonum ATCC 27637 and Bacteroides thetaiotaomicron ATCC 29148 into Escherichia coli RR-1, using promoter probe plasmid pK01, carrying a beta-galactosidase (EC-3.2.1.23) gene (galK). About 10% of clones contained promoters functional in E. coli. Plasmid pRCL101, which directed expression of beta-galactosidase to 977 U, and had an insert of 88 bp, was sequenced. 5 Putative -10 sequences and 1 putative -35 sequence were found. The fragment originated from C. absonum DNA. Transcription in vitro showed that there were 2 transcription start sites near the end of the 88 bp sequence, and that C. absonum RNA-polymerase (EC-2.7.7.6) recognized the DNA fragment as an initiation point for transcription. A translation start site was found followed by an open reading frame. From a primer extension assay, 2 transcription initiation sites were found downstream from the 88 bp sequence. This method for promoter isolation may also assure efficient expression of genes in E. coli as well as Clostridium sp., a factor which may be important for large scale protein production in E.coli. (20 ref)
E.C. NUMBERS: 3.2.1.23; 2.7.7.6
DESCRIPTORS: anaerobe Clostridium absonum, Bacteroides thetaiotaomicron promoter, cloning, plasmid pRCL101, DNA sequence bacterium
SECTION: Microbiology-Genetics (A1)

2/9/67 (Item 9 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0070964 DBR Accession No.: 88-01312
Characterization of the tetanus toxin promoter **and expression of nontoxic fragments in E. coli - RNA-polymerase isolation and characterization from** Clostridium **tetani and Escherichia coli (conference abstract)**
AUTHOR: Eisel U; Binz T; Niemann H
CORPORATE SOURCE: Institut fuer Medizinische Virologie, Frankfurter Str. 107, D-6300 Giessen, Germany.
JOURNAL: Biol.Chem.Hoppe Seyler (368, 9, 1037-38) 1987
CODEN: BCHSEI
LANGUAGE: English

ABSTRACT: The tetanus toxin promoter has been characterized. RNA-polymerase (EC-2.7.7.6) was isolated from Clostridium tetani toxigenic strain E88, nontoxigenic variant EK11, and Escherichia coli. RNA-polymerase from EK11 was as efficient in transcription from the toxin promoter as that from strain E88. A region upstream from the transcription start point showed close homology with promoter sequences of other Gram-positive organisms and the E. coli lac promoter. The promoter region and various truncated forms were inserted upstream from the chloramphenicol-acetyltransferase (CAT) gene, and the CAT activity of E. coli lyzates was studied to determine the strength of individual promoters. An A+T-rich region upstream of the toxin promoter was found to have an enhancing effect on the transcription rate in E. coli. Individual toxin-specific peptides spanning the whole toxin molecule have been expressed in E. coli. Fusion proteins with the MS-2 polymerase were synthesized using the pEx31 expression system, and the products were characterized with respect to immunogenicity. (1 ref)
E.C. NUMBERS: 2.7.7.6
DESCRIPTORS: Clostridium tetani tetanus toxin promoter characterization, RNA-polymerase isol., characterization, Escherichia coli bacterium enzyme EC-2.7.7.6
SECTION: Pharmaceuticals-Vaccines; Microbiology-Genetics (D4,A1)

2/9/68 (Item 1 from file: 51)
DIALOG(R)File 51:Food Sci.&Tech.Abs

00758395 1998-05-c0510 SUBFILE: FSTA
Identification and characterization of sporulation-dependent promoters **upstream of the enterotoxin gene (cpe) of** Clostridium perfringens .
Yuling Zhao; Melville, S. B.
Correspondence (Reprint) address, S. B. Melville, Dep. of Microbiol. & Immunol., Univ. of Tennessee, Memphis, TN 38163, USA. Tel. (901) 448-6779. Fax (901) 448-8462. E-mail sbmelville(a)utmem1.utmem.edu
Journal of Bacteriology 1998 , 180 (1) 136-142
NOTE: 30 ref.
DOCUMENT TYPE: Journal Article ISSN: 0021-9193
LANGUAGE: English
In Clostridium perfringens, CPE enterotoxin synthesis is linked with sporulation. Although several apparent mRNA 5' ends have been identified in the region immediately upstream of the cpe gene, the promoters responsible for sporulation-dependent regulation of cpe have not been identified. To determine if these 5' ends represent actual promoter elements, a series of mutational and biochemical analyses of transcription of the upstream region were carried out. 3 promoter sites (P1-3) responsible for CPE synthesis were identified. DNA sequences upstream of P1 were similar to consensus SigK-dependent promoters, while P2 and P3 were similar to consensus SigE-dependent promoters. SigE and SigK are both sporulation-associated sigma factors which are active in the mother cell compartment of sporulating cells of Bacillus subtilis, the same compartment in which CPE is synthesized in C. perfringens.
DESCRIPTORS (HEADINGS): CLOSTRIDIUM; ENTEROTOXINS; FOOD SAFETY; GENETICS
DESCRIPTORS: GENES; PROMOTERS
SECTION HEADINGS: Hygiene & to

ExPASy Home page | Site Map | Search ExPASy | Contact us | Proteomics tools | Swiss-Prot

Search Swiss-Prot/TrEMBL for clostridium perfringens to Go Clear

==========

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query: 30 AA
Date run: 2005-02-15 12:40:58 UTC+0100 on sib-gm1.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,794,555 sequences; 574,459,479 total letters
UniProt Release 4.1 consists of: Swiss-Prot Release 46.1 of 15-Feb-2005: 170140 en
TrEMBL Release 29.1 of 15-Feb-2005: 1614107 entrie

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query
Select up to...

☐ Include query sequence

	Db	AC	Description	Score	E-value
☐	tr	Q83U44	_CLOPE Beta2-toxin [cpb2] [Clostridium perfringens]	101	2e-21
☐	tr	O86264	_CLOPE Beta 2 toxin precursor [Clostridium perfringens C]	101	2e-21
☐	tr	Q93MD0	_CLOPE Beta2-toxin [cpb2] [Clostridium perfringens]	95	1e-19
☐	tr	Q8U1W2	_PYRFU Hypothetical protein PF1092 [PF1092] [Pyrococcus...	32	1.1
☐	sp	P45963	ACR7_CAEEL Acetylcholine receptor, alpha-type subunit ...	32	1.5
☐	tr	Q81L65	_BACAN Iron compound ABC transporter, iron compound-bin...	32	1.5
☐	tr	Q731T5	_BACC1 HlyC domain protein [BCE4080] [Bacillus cereus (...	32	1.5
☐	tr	Q8AWN0	_9SMEG Rhodopsin (Fragment) [Rhod] [Spinachia spinachia]	31	2.0

☐	tr Q65ZZ8 _BORGA	Hypothetical protein [BG0800] [Borrelia garinii]	31	2.0
☐	tr Q5NER8 _FRATT	Hypothetical protein [FTT1550] [Francisella tula...	31	2.7
☐	tr O33865 _BACPU	Plasmid pSH1452, Rep [Bacillus pumilus (Bacillus...	30	3.6
☐	tr Q91F76 _IRV6	450L [Chilo iridescent virus (CIV) (Insect irides...	30	4.8
☐	tr Q72MW1 _LEPIC	Hypothetical protein [LIC13078] [Leptospira inte...	30	4.8
☐	tr Q6LF23 _PLAF7	Hypothetical protein [PFF1215w] [Plasmodium falc...	30	4.8
☐	tr Q73K80 _TREDE	FMN-binding domain protein [TDE2340] [Treponema ...	29	6.4
☐	tr Q8AWP8 _9TELE	Rhodopsin (Fragment) [Rhod] [Ceratias holboelli]	29	8.6
☐	tr Q8AWL3 _PHOGU	Rhodopsin (Fragment) [Rhod] [Pholis gunnellus (B...	29	8.6
☐	tr Q8AWJ5 _9PERO	Rhodopsin (Fragment) [Rhod] [Mene maculata]	29	8.6
☐	tr Q69BZ0 _CYCLU	Rhodopsin (Fragment) [Rhod] [Cyclopterus lumpus ...	29	8.6
☐	tr Q69BX5 _9PERC	Rhodopsin (Fragment) [Rhod] [Triacanthodes sp. A...	29	8.6
☐	tr Q46102 _CAMJE	CdtC (Cytolethal distending toxin C) [cdtC] [Cam...	29	8.6
☐	tr Q64TC5 _BACFR	Hypothetical protein [BF2505] [Bacteroides fragi...	29	8.6
☐	tr Q8A943 _BACTN	Hypothetical protein [BT0974] [Bacteroides theta...	29	8.6
☐	tr Q5HX88 _CAMJE	Cytolethal distending toxin, subunit C [cdtC] [C...	29	8.6
☐	tr Q7B3S5 _CAMJE	CdtC protein (Fragment) [cdtC] [Campylobacter je...	29	8.6

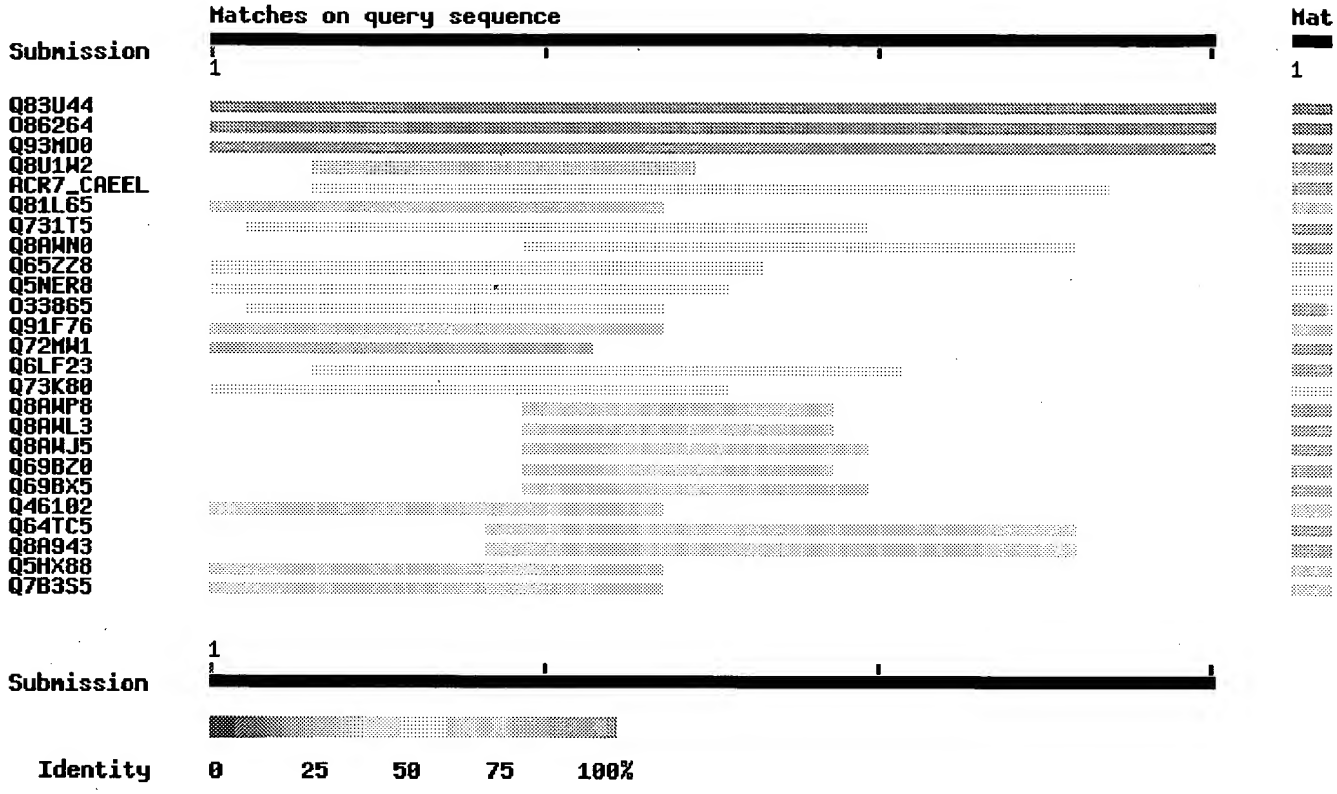
Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits



Alignments

tr Q83U44 **Beta2-toxin [cpb2] [Clostridium perfringens]** 265 AA
Q83U44_CLOPE

align

Score = 101 bits (231), Expect = 2e-21
Identities = 30/30 (100%), Positives = 30/30 (100%)

```
Query: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
          MKKIISKFTVIFMFSCFLIVGAISPMKASA
Sbjct: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
```

tr O86264 **Beta 2 toxin precursor [Clostridium perfringens C]** 265 AA
O86264_CLOPE

align

Score = 101 bits (231), Expect = 2e-21
Identities = 30/30 (100%), Positives = 30/30 (100%)

```
Query: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
          MKKIISKFTVIFMFSCFLIVGAISPMKASA
Sbjct: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
```

tr Q93MD0 Q93MD0_CLOPE **Beta2-toxin [cpb2] [Clostridium perfringens]** 265 AA

align

Score = 95.2 bits (217), Expect = 1e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

```
Query: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
          MKKIISKFTVIFMFS FLIVGAISPMKASA
Sbjct: 1  MKKIISKFTVIFMFSYFLIVGAISPMKASA 30
```

tr Q8U1W2 Q8U1W2_PYRFU **Hypothetical protein PF1092 [PF1092] [Pyrococcus furiosus]** 389 AA

align

Score = 32.0 bits (68), Expect = 1.1
Identities = 9/12 (75%), Positives = 9/12 (75%)

```
Query: 4   IISKFTVIFMFS 15
           II  F VIFMFS
Sbjct: 99  IIATFPVIFMFS 110
```

sp P45963 ACR7_CAEEL **Acetylcholine receptor, alpha-type subunit acr-7 precursor [acr-7] [Caenorhabditis elegans]** 538 AA

align

Score = 31.6 bits (67), Expect = 1.5
Identities = 12/24 (50%), Positives = 14/24 (58%), Gaps = 3/24 (12%)

```
Query: 4   IISKFTVIFMFSCFLIVGAISPMK 27
           II  FT++F   CF  V AI P K
Sbjct: 515 II--FTIVFIICCFIFV-AIPPIK 535
```

tr Q81L65 Q81L65_BACAN **Iron compound ABC transporter, iron compound-binding protein [BA4766] [Bacillus anthracis]** 324 AA

align

Score = 31.6 bits (67), Expect = 1.5
Identities = 9/14 (64%), Positives = 11/14 (78%)

```
Query: 1  MKKIISKFTVIFMF 14
          MKKI S F V+F+F
Sbjct: 1  MKKILSIFIVVFLF 14
```

tr Q731T5 Q731T5_BACC1 **HlyC domain protein [BCE4080] [Bacillus cereus (strain ATCC 10987)]** 99 AA

align

Score = 31.6 bits (67), Expect = 1.5
Identities = 14/26 (53%), Positives = 14/26 (53%), Gaps = 9/26 (34%)

```
Query: 2  KKIISK------FTVI-FMFSCFLIV 20
          KKI  K      F VI FMFSC  IV
Sbjct: 60 KKIFPKKYYIEIFRVIVFMFSC--IV 83
```

tr Q8AWN0 Q8AWN0_9SMEG **Rhodopsin (Fragment) [Rhod] [Spinachia spinachia]** 253 AA
align

Score = 31.2 bits (66), Expect = 2.0
Identities = 10/18 (55%), Positives = 11/18 (60%), Gaps = 6/18 (33%)

```
Query: 10  VIFMFSC-FLIVGAISPM 26
          VI+MF C FLI     PM
Sbjct: 160 VIYMFTCHFLI-----PM 172
```

tr Q65ZZ8 Q65ZZ8_BORGA **Hypothetical protein [BG0800] [Borrelia garinii]** 186 AA
align

Score = 31.2 bits (66), Expect = 2.0
Identities = 10/17 (58%), Positives = 11/17 (63%), Gaps = 3/17 (17%)

```
Query: 1  MKKIISKFTVIFMFSCF 17
          M KI SKF   F+F CF
Sbjct: 1  MNKILSKF---FLFFCF 14
```

tr Q5NER8 Q5NER8_FRATT **Hypothetical protein [FTT1550] [Francisella tularensis (subsp. tularensis)]** 180 AA
align

Score = 30.8 bits (65), Expect = 2.7
Identities = 11/20 (55%), Positives = 11/20 (55%), Gaps = 4/20 (20%)

```
Query: 1  MKKIISKFTVIFM----FSC 16
          MKK ISK  VI M    F C
Sbjct: 1  MKKLISKIGVIIMALGLFGC 20
```

tr O33865 O33865_BACPU **Plasmid pSH1452, Rep [Bacillus pumilus (Bacillus mesentericus)]** 177 AA
align

Score = 30.3 bits (64), Expect = 3.6
Identities = 10/20 (50%), Positives = 11/20 (55%), Gaps = 7/20 (35%)

```
Query: 2  KKIIS-------KFTVIFMF 14
          KKIIS        F V+FMF
Sbjct: 4  KKIISLITILVLTFSVVFMF 23
```

tr Q91F76 Q91F76_IRV6 **450L [Chilo iridescent virus (CIV) (Insect iridescent virus type 6)]** 74 AA align

```
 Score = 29.9 bits (63), Expect = 4.8
 Identities = 9/14 (64%), Positives = 9/14 (64%), Gaps = 4/14 (28%)

Query: 1  MKKIISKFTVIFMF 14
          MKKI    T IFMF
Sbjct: 1  MKKI----TMIFMF 10
```

tr Q72MW1 Q72MW1_LEPIC **Hypothetical protein [LIC13078] [Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhageni)]** 289 AA align

```
 Score = 29.9 bits (63), Expect = 4.8
 Identities = 10/12 (83%), Positives = 10/12 (83%)

Query: 1  MKKIISKFTVIF 12
          MKKIIS F VIF
Sbjct: 15 MKKIISLFFVIF 26
```

tr Q6LF23 Q6LF23_PLAF7 **Hypothetical protein [PFF1215w] [Plasmodium falciparum (isolate 3D7)]** 413 AA align

```
 Score = 29.9 bits (63), Expect = 4.8
 Identities = 12/22 (54%), Positives = 14/22 (63%), Gaps = 6/22 (27%)

Query: 4   IISKFTVIFMFSCF----LIVG 21
           II KF +IF FSCF     I+G
Sbjct: 243 II-KF-IIFTFSCFIYAIIIIG 262
```

tr Q73K80 Q73K80_TREDE **FMN-binding domain protein [TDE2340] [Treponema denticola]** 120 AA align

```
 Score = 29.5 bits (62), Expect = 6.4
 Identities = 11/22 (50%), Positives = 13/22 (59%), Gaps = 8/22 (36%)

Query: 1  MKKIISKFTVI------FMFSC 16
          MKKI   FT+I      F+FSC
Sbjct: 1  MKKIC--FTIIVFALSIFLFSC 20
```

tr Q8AWP8 Q8AWP8_9TELE **Rhodopsin (Fragment) [Rhod] [Ceratias holboelli]** 253 AA
align

Score = 29.1 bits (61), Expect = 8.6
Identities = 8/11 (72%), Positives = 10/11 (90%), Gaps = 1/11 (9%)

```
Query: 10  VIFMFSC-FLI 19
           VI+MFSC FL+
Sbjct: 160 VIYMFSCHFLV 170
```

tr Q8AWL3 Q8AWL3_PHOGU **Rhodopsin (Fragment) [Rhod] [Pholis gunnellus (Butterfish) (Rock gunnel)]** 249 AA
align

Score = 29.1 bits (61), Expect = 8.6
Identities = 8/11 (72%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

```
Query: 10  VIFMFSC-FLI 19
           VI+MF C FLI
Sbjct: 156 VIYMFTCHFLI 166
```

tr Q8AWJ5 Q8AWJ5_9PERO **Rhodopsin (Fragment) [Rhod] [Mene maculata]** 253 AA
align

Score = 29.1 bits (61), Expect = 8.6
Identities = 10/16 (62%), Positives = 11/16 (68%), Gaps = 5/16 (31%)

```
Query: 10  VIFMFSC-FL----IV 20
           VI+MFSC FL    IV
Sbjct: 160 VIYMFSCHFLTPLTIV 175
```

tr Q69BZ0 Q69BZ0_CYCLU **Rhodopsin (Fragment) [Rhod] [Cyclopterus lumpus (Lumpsucker)]** 252 AA
align

Score = 29.1 bits (61), Expect = 8.6
Identities = 8/11 (72%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

```
Query: 10  VIFMFSC-FLI 19
           VI+MF C FLI
Sbjct: 160 VIYMFTCHFLI 170
```

tr Q69BX5 **Rhodopsin (Fragment) [Rhod] [Triacanthodes sp. AD-2003]** 216 AA

Q69BX5_9PERC

align

Score = 29.1 bits (61), Expect = 8.6
Identities = 10/16 (62%), Positives = 11/16 (68%), Gaps = 5/16 (31%)

```
Query: 10  VIFMFSC-FL----IV 20
           VI+MFSC FL    IV
Sbjct: 123 VIYMFSCHFLTPLTIV 138
```

tr Q46102 Q46102_CAMJE **CdtC (Cytolethal distending toxin C) [cdtC] [Campylobacter jejuni]** 189 AA align

Score = 29.1 bits (61), Expect = 8.6
Identities = 9/14 (64%), Positives = 9/14 (64%), Gaps = 3/14 (21%)

```
Query: 1  MKKIISKFTVIFMF 14
          MKKII   T  FMF
Sbjct: 1  MKKII---TLFFMF 11
```

tr Q64TC5 Q64TC5_BACFR **Hypothetical protein [BF2505] [Bacteroides fragilis]** 161 AA align

Score = 29.1 bits (61), Expect = 8.6
Identities = 11/18 (61%), Positives = 11/18 (61%), Gaps = 4/18 (22%)

```
Query: 9   TVIFMFSCFLIVGAISPM 26
           TVIFM    L VGA  PM
Sbjct: 135 TVIFM----LAVGATFPM 148
```

tr Q8A943 Q8A943_BACTN **Hypothetical protein [BT0974] [Bacteroides thetaiotaomicron]** 164 AA align

Score = 29.1 bits (61), Expect = 8.6
Identities = 11/18 (61%), Positives = 11/18 (61%), Gaps = 4/18 (22%)

```
Query: 9   TVIFMFSCFLIVGAISPM 26
           TVIFM    L VGA  PM
Sbjct: 138 TVIFM----LAVGATFPM 151
```

tr Q5HX88 Q5HX88_CAMJE **Cytolethal distending toxin, subunit C [cdtC] [Campylobacter jejuni RM1221]** 189 AA align

Score = 29.1 bits (61), Expect = 8.6

Identities = 9/14 (64%), Positives = 9/14 (64%), Gaps = 3/14 (21%)

```
Query: 1  MKKIISKFTVIFMF 14
          MKKII   T  FMF
Sbjct: 1  MKKII---TLFFMF 11
```

tr Q7B3S5 **CdtC protein (Fragment) [cdtC] [Campylobacter jejuni]** 111 AA
Q7B3S5_CAMJE

align

Score = 29.1 bits (61), Expect = 8.6
Identities = 9/14 (64%), Positives = 9/14 (64%), Gaps = 3/14 (21%)

```
Query: 1  MKKIISKFTVIFMF 14
          MKKII   T  FMF
Sbjct: 1  MKKII---TLFFMF 11
```

Database: EXPASY/UniProt
Posted date: Feb 15, 2005 11:36 AM
Number of letters in database: 574,459,479
Number of sequences in database: 1,794,555

Lambda	K	H
0.343	0.274	1.80

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
length of query: 30
length of database: 574,459,479
effective HSP length: 21
effective length of query: 9
effective length of database: 536,773,824
effective search space: 4830964416
effective search space used: 4830964416
T: 16
A: 40
X1: 15 (7.4 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 40 (21.6 bits)
S2: 61 (29.1 bits)

Wallclock time: 2 seconds

NiceProt View of TrEMBL: O86264

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**O86264_CLOPE**
Primary accession number	**O86264**
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 24, June 2003

Name and origin of the protein

Protein name	**Beta 2 toxin [Precursor]**
Synonyms	None
Gene name	None
From	Clostridium perfringens C [TaxID: 79668]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

[1] NUCLEOTIDE SEQUENCE.
STRAIN=CWC245;
DOI=10.1016/S0378-1119(97)00493-9;MEDLINE=98085977;PubMed=9426008 [NCBI, ExPASy, EBI, Israel, Japan]
Gibert M., Jolivet-Reynaud C., Popoff M.R.;
"Beta2 toxin, a novel toxin produced by Clostridium perfringens.";
Gene 203:65-73(1997).

[2] NUCLEOTIDE SEQUENCE.
STRAIN=CWC245;
Popoff M.R.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

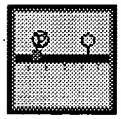
EMBL	L77965; AAC27654.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	JC6515; JC6515.

ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	O86264.
PRESAGE	O86264.
ModBase	O86264.
SMR	O86264; 8972E69F52B26CBD.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Signal.

Features

 Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	30	30	*Potential.*
CHAIN	31	265	235	beta 2 toxin.

Sequence information

Length: **265 AA** [This is the length of the unprocessed precursor]

Molecular weight: **30963 Da** [This is the MW of the unprocessed precursor]

CRC64: **8972E69F52B26CBD** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
MKKIISKFTV IFMFSCFLIV GAISPMKASA KEIDAYRKVM ENYLNALKNY DINTVVNISE

        70         80         90        100        110        120
DERVNNVEQY REMLEDFKYD PNQQLKSFEI LNSQKSDNKE IFNVKTEFLN GAIYDMEFTV

       130        140        150        160        170        180
SSKDGKLIVS DMERTKVENE GKYILTPSFR TQVCTWDDEL AQAIGGVYPQ TYSDRFTYYA

       190        200        210        220        230        240
DNILLNFRQY ATSGSRDLKV EYSVVDHWMW KDDVKASQMV YGQNPDSARQ IRLYIEKGQS

       250        260
FYKYRIRIKN FTPASIRVFG EGYCA
```

O86264 in FASTA format

View entry in original TrEMBL format
View entry in raw text format (no links)
Request for annotation of this TrEMBL entry

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

```
SYSTEM:OS  - DIALOG OneSearch
  File 155:MEDLINE(R) 1951-2005/Feb W2
         (c) format only 2005 The Dialog Corp.
*File 155: Medline has resumed updating. Please see
HELP NEWS 155 for details.
  File   5:Biosis Previews(R) 1969-2005/Feb W1
         (c) 2005 BIOSIS
*File   5: Price change effective Jan 1, 2005. Enter HELP
RATES 5 for details.
  File 390:Beilstein Facts  Nov. 2004
         (c) 2005 Beilstein GmbH
*File 390: File has been reloaded. Please see HELP NEWS 390.
IMPORTANT - Price based on output.  See HELP RATES 390.
  File 399:CA SEARCH(R) 1967-2005/UD=14207
         (c) 2005 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
Alert feature enhanced for multiple files, etc. See HELP ALERT.
  File  34:SciSearch(R) Cited Ref Sci 1990-2005/Feb W1
         (c) 2005 Inst for Sci Info
*File  34: Price change effective Jan 1, 2005. Enter HELP
RATES 34 for details.
  File  73:EMBASE 1974-2005/Feb W1
         (c) 2005 Elsevier Science B.V.
*File  73: Price change effective Jan 1, 2005. Enter HELP
RATES 73 for details.
  File 144:Pascal 1973-2005/Feb W1
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*File 144: Price change effective Jan 1, 2005. Enter HELP
RATES 144 for details.
  File 357:Derwent Biotech Res. _1982-2005/Feb W2
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  File  71:ELSEVIER BIOBASE 1994-2005/Feb W1
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  File 143:Biol. & Agric. Index 1983-2005/Jan
         (c) 2005 The HW Wilson Co
  File  51:Food Sci.&Tech.Abs 1969-2005/Feb W2
         (c) 2005 FSTA IFIS Publishing
  File 156:ToxFile 1965-2005/Feb W1
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*File 156: Updating of ToxFile has resumed, with
UD=20041205.
  File 484:Periodical Abs Plustext 1986-2005/Feb W1
         (c) 2005 ProQuest
*File 484: SELECT IMAGE AVAILABILITY FOR PROQUEST FILES
ENTER 'HELP PROQUEST' FOR MORE
  File  98:General Sci Abs/Full-Text 1984-2004/Sep
         (c) 2004 The HW Wilson Co.
  File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
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RATES 434 for details.
  File 453:Drugs of the Future 1990-2002/Oct
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*File 453: Updating of this file has temporarily ceased due to
a production system change.
  File 286:Biotechnology Directory Current Jan B2
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*File 286: Price change effective Jan 1, 2005.
Enter HELP RATES286 after 1/1/2005 for more information.
  File   8:Ei Compendex(R) 1970-2005/Jan W3
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*File   8: Price change effective Jan 1, 2005. Enter HELP
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  File  35:Dissertation Abs Online 1861-2005/Jan
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  File  50:CAB Abstracts 1972-2005/Jan
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File 155:MEDLINE(R) 1951-2005/Feb W2
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*File 155: Medline will be reloaded shortly and accession numbers will change.
File 5:Biosis Previews(R) 1969-2005/Feb W2
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*File 5: Price change effective Jan 1, 2005. Enter HELP RATES 5 for details.
File 34:SciSearch(R) Cited Ref Sci 1990-2005/Feb W2
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*File 34: Price change effective Jan 1, 2005. Enter HELP RATES 34 for details.
File 35:Dissertation Abs Online 1861-2005/Jan
(c) 2005 ProQuest Info&Learning
File 48:SPORTDiscus 1962-2005/May
(c) 2005 Sport Information Resource Centre
File 65:Inside Conferences 1993-2005/Feb W2
(c) 2005 BLDSC all rts. reserv.
File 71:ELSEVIER BIOBASE 1994-2005/Feb W1
(c) 2005 Elsevier Science B.V.
File 73:EMBASE 1974-2005/Feb W1
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*File 73: Price change effective Jan 1, 2005. Enter HELP RATES 73 for details.
File 91:MANTIS(TM) 1880-2005/Feb
2001 (c) Action Potential
File 94:JICST-EPlus 1985-2005/Jan W1
(c)2005 Japan Science and Tech Corp(JST)
File 98:General Sci Abs/Full-Text 1984-2004/Sep
(c) 2004 The HW Wilson Co.
File 135:NewsRx Weekly Reports 1995-2005/Feb W1
(c) 2005 NewsRx
*File 135: New newsletters are now added. See Help News135 for the complete list of newsletters.
File 144:Pascal 1973-2005/Feb W1
(c) 2005 INIST/CNRS
*File 144: Price change effective Jan 1, 2005. Enter HELP RATES 144 for details.
File 149:TGG Health&Wellness DB(SM) 1976-2005/Feb W1
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File 156:ToxFile 1965-2005/Feb W2
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*File 156: Updating of ToxFile has resumed, with UD=20041205.
File 159:Cancerlit 1975-2002/Oct
(c) format only 2002 Dialog Corporation
*File 159: Cancerlit is no longer updating.
Please see HELP NEWS159.
File 162:Global Health 1983-2005/Jan
(c) 2005 CAB International
File 164:Allied & Complementary Medicine 1984-2005/Feb
(c) 2005 BLHCIS
File 172:EMBASE Alert 2005/Feb W1
(c) 2005 Elsevier Science B.V.
*File 172: Price change effective Jan 1, 2005. Enter HELP RATES 172 for details.
File 266:FEDRIP 2004/Nov
Comp & dist by NTIS, Intl Copyright All Rights Res
File 369:New Scientist 1994-2005/Jan W5
(c) 2005 Reed Business Information Ltd.
File 370:Science 1996-1999/Jul W3
(c) 1999 AAAS
*File 370: This file is closed (no updates). Use File 47 for more current information.
File 399:CA SEARCH(R) 1967-2005/UD=14207
(c) 2005 American Chemical Society

210 215 220

Pro Asp Ser Ala Arg Gln Ile Arg Leu Tyr Ile Glu Lys Gly Gln Ser
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	Q46102_CAMJE	**[Campylobacter jejuni]**	AA
			align

Score = 29.1 bits (61), Expect = 8.6
Identities = 9/14 (64%), Positives = 9/14 (64%), Gaps = 3/14 (21%)

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Sbjct: 1  MKKII---TLFFMF 11
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aa encoded by SEQ ID NO: 4

Reference Disclosure